

GenCore version 5.1.6  
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On protein - protein search, using sw model

Run on : August 19, 2003, 15:17:50 ; Search time 43 Seconds  
(without alignments)  
1693.016 Million cell updates/sec

Title: US-09-494-297-2  
Perfect score: 3945  
Sequence: 1 MKKTRFPNKLNTLNTQRLS.....IAGISLGIWGIHTRIRKHD 757  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

## RESULT 1

S40043 adhesin - Streptococcus pyogenes

C;Species: Streptococcus pyogenes  
C;Accession: S40043

R;Sela, S.; Aviv, A.; Tovi, A.; Burstein, I.; Caparon, G.; Hanski, E.

Mol. Microbiol. 10, 1049-1055, 1993

A;Title: Protein F, an adhesin of Streptococcus pyogenes binds fibronectin via two di

A;Reference number: S40043; MUID:95020565; PMID:7934855

A;Accession: S40043

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: GB:L10919; NID:9425479; PIDN:AAA26954.1; PID:9425480

Query Match

16.1%; Score 633.5; DB 2; Length 659;

Matches 203; Conservative 128; Mismatches 237; Indels 211; Gaps 30;

Qy 20 SKNSKREVVTLVGVFILMFALVTSMVGAKTVGLVFEESTPNAINPPOSSEFRWYGYESVY 79

Db 24 TKKRKFRAVTLYGVFFMLACAGAIGFCGVOVAADEKTVPHSSP-NPEFPWYGDAYG 81

Qy 80 RGHPIYKOFVRVADHLRNLLEGRSYQYCFCNLUKKAFPLGLSDSVKKYKHHGDISIKFED 139

Db 82 KEYPPGYNWTRHDLRNYNGRSYQYCVENNTSINPSQSKETIKKEFNGISFVD 141

Qy 140 YAMSPRTGDELNUKLRAVMYNGHQNANGTIMEGLERLNATRVTEQAEWVYSDNAPTSNP 199

Db 142 YAHTTKLGKEELERQLLSSLNLYNAPNDANGYMGKGLERLNATRVTOAWHSDNSQYQF- 200

Qy 200 DESFKRSESNLVTSOLSLMSQALKOLIDPLATKPKQVEDDPLSIFSESKDKYK 259

Db 201 ETIWESEAKEGKTSRQVTLMRREALKKLUDPMLATEAVNKLFPSGYRNIFEE-----N 254

Qy 260 KQYQNLISGGGLYPTKPTPGDPMPMPNQPOQTNSVLIKYAIGDYSKLEGATL---QLT 315

Db 255 EAYGPNLISAEXYVPPDPKPGE--TSEINPKPPE-----LDGPPIPDEPKHP 298

Qy 316 GDNVNSFQARVESSNDIGERIFLSDGTYTFLNNSPAGYSTAEPITFVKVEAGKVYTDG 375

Db 299 DNLNEPLTPPVMDL--GEEV-----PEVPSELEPAUPLPME-----LDG 337

Qy 376 KQIENPNEKIVE-PYSVEAANDFERSVLTTONYKTYYAKNKGSSQVYCFNADLKP 434

Db 338 QEV--PEKPSIDLPIEVPRYE-----FNKDQSP 364

Qy 435 PDSEGGKTMPDFITGEVKY-THIAGRDLKFTVPRDTPDFTFLKHKKVIEKOREK 493

Db 365 LAGE-----SGETEITEVGNQ----QNPVIDRK-----KLPNFGF-S 399

bacillopeptidase F  
toxin B - Clostrid  
surface lipoprotein  
adhesin homolog Im  
hypothetical prote  
probable peptidol  
hypothetical prote  
hypothetical prote  
large repetitive p  
hypothetical prote  
fibronectin-bindin  
hypothetical prote  
surface-layer 125K  
hypothetical prote  
hypothetical prote  
chaperone and heat

QY 494 GQAIEYSGLTETQLRAATQLAIYVITDSAELEKDKLKDVKDYG-----FG 536  
 Db 400 GNMVETEDTKEPEVLMGGQ-----SESVPTKDQTGMSGQTPOVETDTKEPEVLMG 453  
 QY 537 DMNDSTLAVAKILVEYAQS-----NPPQTLDDFFPLNNNKYQSLIGCTQWHPEPDLV 589  
 Db 454 GQSES-----VEFTKPROTGMSGQTPOVETDTKEPE----- 486  
 QY 590 TIRMEDKKEVTPVTHNLTRKTVTLAGDRMKDFHFEELKKNKO-ELL-----SOTVKTID 644  
 Db 487 -VLMGGQSESVEFT-----KDTQTMGSQFTP-----QVETEDTKEPEVLMGGQSESVEFT 536  
 QY 645 KTNLERFKDGATINLKHGESLTDQLPGEYSVYLKETDSEGYKVKNSEVANATVSKTG 704  
 Db 537 KDTQTMGSQOPTPOETEDTKEPEVLMGGQSESVEFT-----KDTQTMGSQFSETA 587  
 QY 705 ITSDT-----LAFFNNK-----EPVVP-TGVDQKINGYALIVLAGISI 743  
 Db 588 TVVEDTRPKLVFHFDNNPKEENREKPTKNITPLPATGDIENVLAFLGILILSVL 646

RESULT 2

S54418 fibronectin-binding protein precursor - *Streptococcus pyogenes*  
 C;Species: *streptococcus pyogenes*  
 C;Accession: 06-Sep-1995 #sequence\_revision 13-Mar-1997 #text\_change 15-Oct-1999  
 R;Palay, S.R.; Valentim-Weigand, P.; Timmis, K.N.; Chhatwal, G.S.  
 MOL: Microbiol. 13: 531-539, 1994  
 A;Title: Domain structure and conserved epitopes of Sfb protein, the fibronectin-binding protein precursor of *Streptococcus pyogenes*.  
 A;Reference number: S54418; MUID:95089690; PMID:7527894  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-638 <TAZ>  
 A;Cross references: EMBL:X67947; NID:9511149; PIDN:CAA48133.1; PID:9511150  
 Infect Immun. 60: 3837-3844, 1992  
 A;Title: Fibronectin-binding protein of *Streptococcus pyogenes*: sequence of the binding protein F2  
 A;Reference number: A44792; MUID:92363585; PMID:1386839  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 371-638 <TAZ>  
 A;Cross references: EMBL:X67947  
 C;Genetics:  
 A;Gene: sfb  
 C;Keywords: fibronectin binding #status predicted <SIG>  
 F;50-638/Product: fibronectin binding protein #status predicted <MAT>

Query Match 15 3%; Score 603; DB 2; Length 638;  
 Best Local Similarity 27.4%; Pred. No. 5.5e-28;  
 Matches 207; Conservative 118; Mismatches 248; Indels 182; Gaps 32;

QY 20 SKNSKRFTLVLGFLMLRLNTWGAIVKVFGLVESSTPNAINDSSSBYRWGYESV 79  
 Db 177 TKRRRFAYLVLGVTFMLASAGAIGFCQVAADEKTFPHRVS-QNFPFWGYDF- 73  
 QY 80 RGHPYKQPRVADLRLVLEGSRSTOYVCPNKLKRAFPPLGSDSSYRKWKHDGSTKFD 139  
 Db 74 KG PYTRY---HNLQNLNLSKTYQAYCFCNLKREPKEGSYFPNWYKRWDGSEETFVK 128  
 QY 140 YAMSP-----RITGDELJNOKLRAVMYGHQPQANGINMEGLDINAIRVQEAWVYSD 192  
 Db 129 YADNPKRDNBRSRVIDVLELKLNILVLYNGYPNNGIMEGLEPLNAILVTONAWYSSD 188  
 QY 193 NAPTSNPDESFKRESESNIVSTSOLSLMPQALKOQLIDPNLATKPKQVDDDFQLSIFEE 252  
 Db 189 NSSTFNNTDNFETTEAKDLNIKPEQSLMLPMVALKLLKPLKSEESLKPVSTFRUNIFESQ 248  
 QY 253 DKGDKYNYKQYONLLSGGLVPTKPTPGDPMPMPQNPQRTTSVLRKIAIDYSKLEGATL 312

RESULT 3

T30856 protein F2 - *Streptococcus pyogenes*  
 C;Species: *streptococcus pyogenes*  
 C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 11-May-2000  
 C;Accession: T30856  
 R;Jaffe, J.; Natanson-Yaron, S.; Caparon, M.G.; Hanski, E.  
 MOL: Microbiol. 21: 373-384, 1996  
 A;Title: Protein F2, a novel fibronectin-binding protein from *Streptococcus pyogenes*,  
 A;Reference number: z20907; MUID:97011581; PMID:8858591  
 A;Accession: T30856  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-1039 <JAF>  
 A;Cross-references: EMBL:U31980; NID:91654115; PID:91654116; PIDN: AAC44522.1  
 C;Genetics:  
 A;Note: PRTF2

Query Match 4 2%; Score 164; DB 2; Length 1039;  
 Best Local Similarity 19.7%; Pred. No. 0.13; Mismatches 279; Indels 296; Gaps 46;  
 Matches 171; Conservative 124; Mismatches 279; Indels 296; Gaps 46;

QY 57 STPNAINP-DSSSERWYGYESVYCHPYKQFRVADLRLVNLLEGSRSQVYCENKKFA 115  
 Db 110 NSPLAIGKYDAKTHOLTYIFTNYAG--LDKVKQSAELSFLNEKVELE----- 156  
 QY 116 PLGSISSSVKKWKKIDGISTKFEDAMSRSITRGEBLNOK--LRAWMYNGHQANANGIMEG 173  
 Db 157 -----NINISDEKF--IGGCEITYKGIVVNLIGNESTKESNITING 196  
 QY 174 L-----EPLNATRVTQEAWVYSSDNABISN-----PDESERRESNLVTS 215  
 Db 197 LSNVCGSIESNT--ETGEFWVYVYVNPNTIPYAVLNWLGFARRTAOGENDNSLVA 254  
 QY 216 QLS-----LMRQALKQLIDPLNATKMP-----KQPDFD-- 244  
 Db 255 QLTGYDIYEVPHNYRLPTSYGVDIRNLK---DLEAKLPOGSTDQANKRRLIDGEN 310

QY 245 ---QISIFEREDKGDKYK-----GYNQNLSSG-----GLVPTKPTP 277  
 : ; : ; : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 311 LOGKEFVVVKYTGKADOSGKELIVOSHLSFNNWGSYKTLRPNSHVSFTNBIALSPSKSG 370  
 QY 278 PGDPMPPPNPQTTSVLIRYKAIGYSKL-----LEGATIQLTCDNVMSQFARFESSND 331  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 371 SGTSEF--TKPSITVANKRVAQLPKKKVSTDNVPLPEAFLRSSNGNS-QKLEASSNT 427  
 QY 332 IGE-RIELSDGTVILTELNSPAGSIA-----EPITP-KVEA 366  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 428 OGELIHKDLISGTYDLYETEAKPGYQQVTEKLATVYDITTPKAECOMVKRKPHSKRYKVEA 487  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 QY 367 GKVYTTID-----GKQIENPNKEIVEDPYSVEA-----NDFEERFSVLNTQNYA 409  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 488 NKEVITIVNKHETLIFSGKKIWEDDRDQRPAKIQVOLLQNCQKMPNOIQE--VIKDNDW 544  
 QY 410 KFYV-----AKNNGSSOVVYCFNADIKSPPOSEDGGK-----TMTPDTGE 452  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 545 SYHFKDLPKYDAKNOEYKSY---AEVKWP---DGKVSYLGNDNFNRETFEEQ 595  
 QY 453 VKYTHIAGROLFKVYKPRTDPPFLKHKHVKVIEG-YREKGQAIETSGLTEQRLA- 509  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 595 NNFNLNEFGWAEIKQSGPKTIDEOTLTSFGKKWKNDAENRQAI-----IVOLYAD 649  
 QY 510 -ATOLAIYIFTDSA---ELDKDKLUDYIGFGDMMDSTIAVAKILVEYAQDSNRPQLTDL 564  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 650 GVAVEGQOTKFISGSNEWSPEFKNUKKYNGT--NDITSVKVEVPTSYD----- 698  
 QY 565 DFFTPNNKVKQSLGTOWHEDLDVITRMEDKKEVTPV-HNLTRLKTV--TGLAGDRT 620  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 699 -----VTVSANDIN---TKREVITQGPNLTEETIPLESAGSGGTT 738  
 QY 621 KDFHEIE-----LANKNQELLSOTVKTDK-TNLIFK---DGK---ATINLKH 661  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 739 -----TVEDSRPVDTLGSQISEQSGQGDWITEEDSATHKFSKRQDIDKELLAGMELRD 793  
 QY 662 GESLTLOG-----LPEGSYSLVKETDSEGYK-----KVNSOEVANATVSKT 703  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 794 SSGKUISTWISDGQVKDFYLMPGKTF-VETAADAYEATAITFTVNEQ--GQVTYNGK 850  
 QY 704 GITSDETLAFENKKEPVVPTG---VDQKI 729  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 851 ATKGDAHIVAWDAYKPTKGSGQVIDEELK 880

**RESULT 4**  
 ACI1533 surface protein (LXKTG motif) [imported] - Listeria innocua (strain Clip1262)  
 C;Species: Listeria innocua  
 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C;Accession: ACI1533  
 R;Glaser, P.; Flangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsilhi, H.; Jones, L.M.; Karst, U.  
 C;Reference number: AB1077; MUID:2153279; PMID:1676669  
 A;Accession: ACI1533  
 A;Status: preliminary  
 A;Title: Comparative genomics of Listeria species  
 A;Reference number: AB1077; MUID:2153279; PMID:1676669

**RESULT 5**  
 S60138 sex factor aggregation protein precursor - Lactococcus lactis  
 C;Species: Lactococcus lactis  
 C;Date: 15-Feb-1995 #sequence\_revision 01-Mar-1996 #text\_change 15-Oct-1999  
 C;Accession: S60138; S49417  
 R;Godon, J.-J.; Jury, K.; Shearman, C.A.; Gasson, M.J.  
 submitted to the EMBL Data Library, December 1993  
 A;Description: The Lactococcus lactis sex-factor aggregation gene cluA.  
 A;Reference number: S60138  
 A;Accession: S60138  
 A;Molecule type: DNA  
 A;Residues: 1-1243 <GOD>  
 A;Cross-references: EMBL:U04468; NID:9458233; PID:AAA66196.1; PID:9458234  
 R;Godon, J.-J.; Jury, K.; Shearman, C.A.; Gasson, M.J.  
 Mol. Microbiol. 12, 655-663, 1994

Query Match 4.1%; Score 161; DB 2; Length 1386;  
 Best Local Similarity 19.7%; Pred. No. 0.3;  
 Matches 163; Conservative 127; Mismatches 301; Indels 238; Gaps 41;

RESULT 6	
A;Title: The Lactococcus lactis sex-factor aggregation gene clua.	A;Reference number: S49417; MUID:95020601; PMID:7934889
A;Accession: S49417	A;Status: nucleic acid sequence not shown
A;Molecule type: DNA	A;Residues: 61-161; 482-487; 489-824 <GOW>
A;Cross-references: EMBL:U04468	C;Genetics:
C;Gene: clua	R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloed, J.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihogios, J.C.; Schleifer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehrlin, A.; Title: comparative genomics of Listeria species
F;1-4-13/Domain: signal sequence #status predicted <SIG>	A;Reference number: AB1077; MUID:21537279; PMID:1679669
Query Match 4.0%; Score 159; DB 2; Length 1243;	A;Status: preliminary
Best Local Similarity 19.6%; Pred. No. 0.33; Matches 160; Conservative 100; Mismatches 243; Indels 314; Gaps 42;	A;Molecule type: DNA
QY 98 LEGSSRSYQWCFNLKKAFFPLGSDDSVKKWKKHHGGISTKFEDYAMSPRITGDELNQKLRA 157	A;Residues: 1-1612 <GLA>
Db 335 MAGSLNYS-----KSKTPPEGGLPPPTSDQYINQHRSVS-FDN-----IL 370	A;Cross-references: GB:NC_003310; PIDN:CAD00256.1; PID:g16411648; GSPPDB:GN00177
QY 158 VMNGHNPONANGIMEGLEPLNATRWTQEAWSYSDNAPISNPDESFKRESESNLVSLSOL 217	A;Experimental source: strain EGD-e
Db 371 VVGSYFPSSGVHKVSG-RPTSGANATGDS--WSSNPPSTNETWSATAVTDYKAIGPS- 424	C;Genetics:
QY 218 SLMRQALKOLIDPNLATK---MPKQVPDFQFOLISIFESEDKGKYYKGYQNL-LSGGL 270	A;Gene: Imo2178
Db 425 -----DVTENMDVGTKNSWYGMNLIPDKGQPSISIV-----ANMVALNGQ 471	Query Match 4.0%; Score 159; DB 2; Length 1612;
QY 271 VPTKRPPTPDPMPMPNNPQPOPTSVLIRKYAIGDYSRKLEGATLQLTGDNNSFQARVFSSN 330	Best Local Similarity 20.9%; Pred. No. 0.5; Matches 184; Conservative 99; Mismatches 320; Indels 278; Gaps 47; Matches 184; Conservative 99; Mismatches 320; Indels 278; Gaps 47;
Db 472 LPNPKIPT-EPPPPPVPKPTAIVYDQAIFQTDNTR-----AVTQDGTDLN----- 516	QY 56 SSTPNAINPDSSSEYKWMYGIYSYVRGHPIYKQFRVADLRLNRLEGSRSYQYCFNLKAF 115
QY 331 DIERRIELSD-GTVTTELNSPAGYASIE-----PITFKVERGKVUTI-----ID 374	Db 825 STKPNE-----NMWFY-SYQVNTAKVDNGV-----EKYSQYQASYKLENAM 867
Db 517 --GALVNKOETENNVWLSNEVLPAGHEVIKSYMTPDLPLEGFKLDEQSNTLSPDVDTLD 574	QY 116 -----PLGDSSSVKKWYKHDGISTKFEYLAMSPPRTG 148
QY 375 GK-----QIENPKKEIVEPYSEVAINDPEEFSLVTTQWAKFTYAKKNNGSSQ 423	Db 868 TKTATIDPSFDNKVNNTVTLNNSISADRPNINPITDPMKIGTGAQVKSSFKVMEETG 927
Db 575 EKTNVTUTLJAYKATRMLKNDLNGAYQVPE-----TLOCQ-----TQDGQ-----TQDGSS- 617	QY 149 DELNQKURAVWYNGHFTONANGIMEGLEPLNIRVQEA----WYSDNAISNP----- 200
QY 424 YVCFNADLKSPPDSEEDGKTMPDFT-TGEVKVTHIAGRDLFKYTVKFRDTPDPTFLKH 481	Db 928 BDIDSKYDITYTDN-NFTIQFDKATADPKVUTYSTITMSGLVNTATATSPDYGSL 985
Db 618 ---FKNDL-----ETLINDYTVNSNEVE-----VHPDPKFKNSN 651	QY 201 -----ESFRRESENVLVTSQLSISMRQALKOLIDPNLATKMPKQVPPDDQLSI 248
QY 482 IKKVTEKSYREKGSOAIE-----VSLGTETO--LRAATOLAIYPTFDA- 522	Db 986 PTMYKSRRTSISPAFTGSGTATGSLT-----VKKDNEK--KLTGAKOTL 1037
Db 652 -----ASGTTINGOGIDVNATNYYKLLWDLSGYKGKIASSEDIVRG-----FYFVDAAP 700	QY 249 FESEDKG----DKYNRKGQYQNLSSG----LVTPKPPTP-----GDP 281
QY 523 -----ELRKDKLHYHG-----FGDMNDSTLAVAKILVE----- 551	Db 1038 LEGDKAQEOATDSDGKVIMMGLQSSKYYKLYTEAFTPGYTISDEYKGKETVTARIAT 1097
Db 701 DVYDVDLKNISYKQSKQEVKGTFAKVYSSVKDAPPAEVQVLAQAKIAPKGQFVYESVDD 760	QY 282 PMPNPQPOPTSVYLIRK--YAGDYSRKLEGATLQLGDNVNSFOARVFSSTDIGEELS 339
QY 552 -----YAQDSNPPQLT-----DIDFFIDPNNNKQQ-----SLI----- 578	Db 1098 VTIENTEQTGSSVLLKEDSATRD--AIAAGEFELONADGTRVADNLVSNAD--GKLEVT 1152
Db 761 PQPFYTYVQVGTGNWETIOPMTPKREGASGAYQNYDQIDFGNSVEGDTWKNNIIVPPKVK 820	QY 340 D--GTYLTIELNSPAGYASIEPITFKVERGKVUTIDKGQIENPKKEIVEPYSEVAINDPEEFSLVTTQWAK-----FNO 1185
QY 579 -----GTOWH-PEDLVITRMEDKEVLPVTHMLTRKTVTG----- 614	Db 1153 DLAPGQYQFVTTKAPIGY-----VLDGA-----FNO 1185
Db 821 QVSVDGGKTIWHDSDLKDLPDTSNQYDVKLDFNFTANGDYTKILLGDNFESSQWTDLAKVT 880	QY 397 FEESFVLTQWAK--FYYRKNGSSQVYCFNADLKSPDSEDGKTMPDFT-- 450
QY 615 -----LAG-----DRTDFHPEELKNNKKQELISQTVTDKTN----- 647	Db 1186 -EAANVTKERAKIGSVVLTKEVDKEDSVKATLSGAEEFELQNAT----GTKVKDNLTNA 1239
Db 881 DKDGNQDGFQKVLNASGKDVTOKFQDKVKEVQIIFTPKLSDITSLASNSDP 940	QY 451 GEVKVYHAGDL-FXYTVKFR---DTDPFLKIKK----VIEKGYKEGQIEYS 500
QY 648 -----LEFKDGKATINLKHGESMTLQGL--PREGSYVLTKEVTDSEGYKVKVNSQEVANA 698	Db 1240 GKEVTDLAPGDKYKEVETKALPGYELDATPVTIFTEFNQATAVNVTRENKARTGSVV-- 1296
Db 941 DRLLTLMFSKD-----VTKGATGAEALANYL--DKEGV-TVAPNIGQL-D 982	QY 501 GITETOLRAATQALAIYFTDSSAEL--DKDKLKDHFQGDM-----NDSSLAVAKILV 550
QY 699 TVKTKGTSDET--LAFENNEKEPVYPTGYDOKINGYL 733	Db 1297 -LTKLDSKSRNLAFEGELQTKLQVLSKDVYTF-FAQGQIQLNAPGDQOLVERKAPT 1354
QY 983 TTTSRT-VIGCDNTKDKITKSNVTKVLPQPLPMINKYV 1018	QY 551 BYAQDSNPPQLOPLDLDFFIPNNKQY-----SLICQWHPB-----DLV 588
QY 1355 GDLDATP---VETIEFQKAP1QVTKNTMSTGSVWJKTGETKALLANATFKL 1409	QY 589 DTTRMDKPKVYPTVHNTI----RKTWTGIA-GD---RHK-----PFHFEFLKN 631

Db 1410 D---EDNN---VTEILTTDASGKLEITNLAPGDYQLIETKAPAGYELDVPVWKTF 1461  
 Qy 632 NKOELLS----QTVKTDKNUNLEFKDGKATNLKRGESLULQGLPPEGYSVLUKEWDEG 685  
 Db 1462 DOKETLQVTKTNLKTVSGKVIAFEVDTKGKV-LAEKEIHT--GI--VGDKYATKAIDI 1517  
 Qy 686 YKV---KVNSOEVANATVSKTGITSDELAFENNEPKPV----- 721  
 Db 1518 YKLTKOPTNKPGVKEVKETKV-----TFVVEKNRKPVWNPDPKPTPKPVDPAAK 1571  
 Qy 722 -----PTGVYDQKINGYLALIVIAGISLGIGIWTIRIK 755  
 Db 1572 PTVKTSLSLPGTDESPIG----LIFTGLFASPMGLFLIRKSK 1608

RESULT 7  
 F82884 hypothetical protein uua45 [imported] - Ureaplasma urealyticum  
 C;Species: Ureaplasma urealyticum  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: F82884  
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 A;Submitted to: GenBank, February 2000  
 A;Description: The complete sequence of Ureaplasma urealyticum. Alternate views of a min  
 A;Reference number: AB2870  
 A;Accession: F82884  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-5005 <GLA>  
 A;Cross-references:  
 A;Experimental source: serovar 3; biovar 1  
 A;Genetics: UU445  
 A;Genetic code: SGC3

Query Match 4.0%; Score 157.5; DB 2; Length 5005;  
 Best Local Similarity 19.8%; Pred. No. 3.6;  
 Matches 158; Conservative 100; Mismatches 285; Indels 253; Gaps 36;  
 Qy 5 RFPNKLNTLNTPVORVLSKNSRFT-----VTL-----VCEVLMIFALVT 42  
 Db 1598 RIKGQNIISPATISDQQRTYKOMATNLTAGLDYEVSTVTKNQTKNSPIT 1657

Qy 43 SMVGAKT---VFGLVESSTPNAINPDSSESYRWIGYESYVRGHPYKQFRVADLRLVN 99  
 Db 1658 GPGIFVTLAPVKIISL-----DPVHENRNTADIKINLR 1694

Qy 100 GSRSIQCVCENLKKAPPLGSDSSVVKWY KHDGISTKEDYAMSPRITGDELNOKLRAV 158  
 Db 1695 -IENIGASLEN-----KDIKFIFKKRNNDGKQISFIHKVTS----- 1728

Qy 159 MYNGHPRONANGIMEGLEPLNAIRVQEOAWYYSDAPISNPDESPKRESSENLYSQLS 218  
 Db 1729 -----ANDANEWEKDLRNREYTLERVVY-----LKURDENQNSVNSSES----- 1768

Qy 219 LMROAIKQLADPNLATKMPKQVPDDFOLSLFESEDKGDKYKNGYQNLSSGLVPTK 278  
 Db 1769 -----DYLDMWIENLNKTEK-----LLPTKPLGI 1793

Qy 279 GDPPMPNPQQTTSVLIRKVAIGDVKLL EGATIQLTGDNVNSFOARVFSSNDTGE-- 334  
 Db 1794 IGAPIKEISDNGAKYQKL-KFAINDFDDVLENKENOTPKF-- NIQPENNNGANLNESEHEG 1849  
 Qy 335 RIELSDG-TYTTELNLSPAGYSIABPITKEVAGVYTIIDGKQJENPNEKEIVE-PYSVE 392  
 Db 1850 KVELIDGQKFVANLNN-----IKVNKEKYKZ--KIVFDEMDQDVGNGVYKIN 1894

Qy 393 AYNDFEE----FSVLTQNYA--KFYVAKNNGSSQVYCFCNAIDLKSPPDSEDGK 442  
 Db 1895 FKNDYKEPNWVYDAVSNTHTQTYVFTNKRAIASFNSNLTDVANKONTINSLOS---R 1950

Qy 443 TMTPDFTTGEVKYTHIAGROLFKYVVKPQTDPTFLKHKRKKVLERGYRERGQATEYSGL 502

Db 1951 VETIQGHFKAKYIISNDRVVWTNTI--PAPTN-----IGNNNNNNIALNFE-L 1995  
 Qy 503 TETQL--RAATOLAIYFTDSAELDKDQLDYHGFDMNDSTLAVAKILVEYAQDSNPP 559  
 Db 1996 NONOLTSNRLYVTFALVY--SKDVNDE-----NIFANMVYIKNNNPQDSTK 2042  
 Qy 560 QLTDLFFIPNNNNKYSLIGTOWHPELDVLDIIRMEDKKEVTPV-----THNLTTRK 610  
 Db 2043 SSTVYDVLKAQNADENKITSLLSHSNQI---FEDKNNHLIKAKISIDEAHDQIINS 2098  
 Qy 611 TWIGLAGDRTKPFEEIELKNNKOEULLSQVTKDKNLEFKDGKATNL----- 660  
 Db 2099 T-----THDYDTLLEKENNEWLWKTOLNL-KPNTKVRKKVNTSKSDTLYGVN 2149  
 Qy 661 -----HGESLTQGLCBEGSVLUKEDEGK-VKVVKNSQEVANATV-SKGITSD 708  
 Db 2150 KDNIVVPINNHNTNDLKTLEKSTLNVKPT---KTNENKNESIRKLMLGFKNTGSSLE 2204  
 Qy 709 ETLA---FENNEPKV 720  
 Db 2205 NKYAKLUVKDNNNQOI 2220

RESULT 8  
 AH1396 peptidoglycan anchored protein (LPXNG motif) [imported] - Listeria monocytogenes (str  
 C;Species: Listeria monocytogenes  
 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001  
 C;Accession: AH1396  
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Bagner, F.; Berche, P.; Bloch, D.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
 A;Title: Comparative genomics of *Listeria* species  
 A;Reference number: AB1077; MUID:21537279; PMID:1679669  
 A;Accession: AH1396  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1530 <GLA>  
 A;Cross-references:  
 A;Experimental source: strain EGD-e  
 A;Genetics:  
 A;Gene: lmo2576

Query Match 4.0%; Score 156; DB 2; Length 1530;  
 Best Local Similarity 20.5%; Pred. No. 0.69;  
 Matches 160; Conservative 78; Mismatches 221; Indels 316; Gaps 38;  
 Qy 193 NAPISNPDESFKR- ESESNLVTSTOSLMSLQALKOLIDPNTLAMPKQVPDDFOLSLIFE 250  
 Db 794 NMPSGEYDLYTGVDDESN-----LEYFQVKFNEINO SYVIK-----YQTAITL 839

Qy 251 SEDK-----GDKYKNGYQNLSSGLVPTK---PPTPGDPPMPNPQDPTSVLIRKVAI 300  
 Db 840 TSDETTTAQIGNSVTFGDNITKGTEKTEKTMIEVITGD---GAGTGTGERGKIIUNLNUVD 896

Qy 301 GDYSKJLEGATLQTLGDNVNSFOARVFSSNDIGERITLSDGTYTTELNSPAGYI--- 356  
 Db 897 ADPSIPLLEGATFDLYA- NDERVDTQTIDKNOVIERDLYVGDYTKVEKSAPEGYVLPtas 955

Qy 357 AEPITPKVE-----AKVYTIID-GKOIEN 380  
 Db 956 TENIQVKLEQDEKVWQVMNEMPKIETGEVHLVKTDKATGATLAGAEFLSYDVKSCAELQN 1015

Qy 381 ---PNKEIV-----EYPSVEAYDFE---EYPSVEAYDFE---EYPSVEAYDFE--- 417  
 Db 1016 GLTTDENGELTHNIDGGSVYKLTKAPEGYVQLKSRTWERSVESQDATEIOAHNEKDL 1075

Qy 418 -----MGSSQV-----YCT----- 427  
 Db 1076 GEAVLTKVDSETNAKLSGAKFNLLNDSGEVQTNJVDENGIEIRVQNLPGDYAQQTEA 1135



Db 1422 DASGNKATQTVNLRIVDTSPITLITNPLTVSIENRKLTQEELYTAGLIGDNIDLA 1481

Oy 176 PLNAIRTYQEAQWYSSNAPNISPNDPESFKR--ESESNLVSTSQLSLMRALKQ---- 226

Db 1482 PQQAVQPKQPAVFTSFSTFGDIASVKAQOVOVNLASSG---NQAPQTINIV 1537

Oy 227 -----LIDPNLATKMPKQPD 242

Db 1538 VDTVGPKIADNVSYHNTKTEAEFFQDARLDVTDDNDDTDLITTSNFAEKVNLINKPG 1597

Oy 243 DQLSITFESEDKGDKYKNGYQNLSSGLVNPKEPTPRDPMPMPPNQROPTSVLIRKTAIGD 302

Db 1598 KVEVITATDIDKGNOTKEITYQVS---KDKPVITADPKI--SYOCKIEVTEANFLSGV 1651

Oy 303 YSKLLEGATOLQITGDWNNSFQARVFSSNDIGERIELSD-GIVTLEUNSPAGY-SIAEPI 360

Db 1652 HAEV---TDELGD-----VKTLSFAKVKDFKVKVGTWT-LNAKDEBYGNTAEPV 1698

Oy 361 TPKV---EAGKVTTIDGKQIENPNKEIVEPYSEANDFREFSVLITQNYAKFYAKN 416

Db 1699 KVSVSIFNKIATPFNNADNKTEAVN---ELPSLESIFKIE-----AKDVLSGN 1744

Oy 417 KNGSSQTYCWNADLKSPPDSE-----DGKG----TMTPDFTG-EVKYTHAG 460

Db 1745 K---LKVTYTPTQTKIGNVNPGEISIKVTTKODSGNIAETTVTTLTICKTGPISKMT--- 1797

Oy 461 RDLFKYWKPRTDPPDFLKHKKVIEKGKQATEYSGLTEQRLRAQALAIY-FT 519

Db 1798 KSTKFLKEWQSKEPNWTFEGIATDVGDMYKNIKS---EVNLIKVGYPFIFTV 1854

Oy 520 DSAELDKKLKDHYHGGDMNDSTLAVAKILVETAQDSNPPQTLDFEFFPNNNKYQSLIG 579

Db 1855 DALGNESSESSLKASTVQITVTSFELTDKLEISYPTGK---ISDKQFLQDIGTKVNSYG 1911

Oy 580 TOWHPEDINDITRMEDKREVTHNIT-----LRKFTV---GLAGDRKDHF 624

Db 1912 T-----VKTNTNLKSKIVDWNKACKYKVVTATNSGGVAEKT--- 1948

Oy 625 FEIELKNNQELSQVWTKDNLER---DGKATINLKHGESITLQGIPEGYSYLV 678

Db 1949 ILLTVKNSDSSIAVPSKDDNNPKAPNPKTGDLMTELINGMMMLIVE---GRNFTR 2005

Oy 679 KETDSEGKVK 689

Db 2006 RKT---KV 2011

RESULT 11  
S70172  
toxin B - Clostridium difficile

C;Species: Clostridium difficile

C;Date: 12-Feb-1998 #text\_change 15-Oct-1999

C;Accession: S70172; S44271

R; von Eichel-Streiber, C.; Meyer zu Heringdorf, D.; Habermann, E.; Sartingen, S.

Mol. Microbiol. 17, 313-321, 1995

A;Title: Closing in on the toxic domain through analysis of a variant Clostridium difficile

A;Reference number: S70172; PMID:96079281; PMID:7494480

A;Accession: S70172

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-267 <CON>

A;Cross-references: EMBL:223277; NID:9761713; PIDN:CAA80815.1; PID:9761714

R;Sartingen, S.; von Eichel Streiber, C.

R;Submitted to the EMBL Data Library, July 1993

A;Description: Cloning and sequencing of an Clostridium difficile toxin B mutant.

A;Reference number: S44271

C;Keywords: cytotoxin

Query Match 3.8% Score 151; DB 2; Length 2367;  
Best Local Similarity 19.9%; Pred. No. 2.7; Mismatches 292; Indels 304; Gaps 42;  
Matches 171; Conservative 94; Mismatches 292; Indels 304; Gaps 42;

Oy 5 REPNKLNLNTQRLV---SKNSKRFVTLVGFVLFMFAUTISMVGAKTVGVLV--SS 57

Db 1568 KEMRKGSNTNTSDMSLFSLESMNKSIIVNFQSONIKFILDANFIISGTTSGIQFICD 1627

Oy 58 TPNAINP-----DSSETRWY-GYESVGRGHPYKQFRVAHDRLRVNLEGSSSYQVCFN 110

Db 1628 ENNIQPVFIKEVILETVLIVGQRQNMIVEEY-----DLDSDDISSIVIN 1676

Oy 111 LKAFAPLGSDSSVKKWHDGISTKFEEDYAMSPRITGDELNOKLRAVMYNGHQ---N 166

Db 1677 FSOQYLGIDSCVNK-----VVISPNIXDEINITPVVETNNTPPEVILD 1722

Oy 167 ANGIMEGLEPLNARVTOEAQWYSSDNPAPISNPDESKRRESNLNUSTSQSLMRALKQ 226

Db 1723 ANYTNEKIN-VNINDLSTRYW-----SNQGND-----ILMSTSEENKVKSR 1767

Oy 227 LI---DDNLTAKPKQVFDQFDSLIFSEKDQD-----KYNQVNLISG- 268

Db 1768 FVNWKDKTLANKL-----FNSDKDOPVSEILSFTPSY--YEDGLGYD 1813

Oy 269 -GLVPTKBPTPGUPPPMPPNQOPOTSVLIRKYAIGDYSKLLEGATLQLTGDNVNSFOARVE 327

Db 1814 LGLV-----SLYNEKFYINFGFMNVG--LIVINDSLYVFKPV- 1850

Oy 328 SSNDIGERIELSUGTYTTELNSPAGY-SIAEPI-----TPKVEAGKV 370

Db 1851 -NNLITGFTVWGDKYVNPINGGA-SIGETIIDDKNYFNGQVLOQGVFSTDFKY 1908

Oy 371 -----TI---IDQRQIENPKETVEP---YSVEAYNDEEFSVLITQY-----AKFY 413

Db 1909 FAPANTLDENLEGEAIDTQKLIDENTYFEDNRYGAVEMKELDGEHMVSPETGAKF 1968

Oy 414 AKKNGSSQVWCNFAD--LKSPPDSEDDGKTMTPDFTGEVKYTHAGR----- 461

Db 1969 GLNQIGDDK--YYFNSDGMQKGFVFSINDNKHVFDDSGVMKVGYTEIDGKHYFAENGEM 2026

Oy 462 -----DLFKVTKPRTDPTDFLKHKKVIEKGKQALEYSGLTEQRLA 513

Db 2027 QIGVENTEDGFKY-----FAHNHEDL--GNEGEBSISYGLINLNPK----- 2066

Oy 514 AIVYFTDSE-----LQDKDQLKDHYHGGDMN-----DSTIAVAKTLV 550

Db 2067 -IVYFDDSFATVVGWQKDLDEGSKYFDEDTAERYIGLSLINDQYYFNDGIMQVGFTI 2125

Oy 551 E-----YAODSNPQOLTLD-----FPIPNNN----- 572

Db 2126 NDKWFYFSDSGIIIESGVONIDDDNFYIIDDNGTVOQIGVFTSDGKYFAPANTVNNDIYQ 2185

Oy 573 --KQSL-----IGTQHMPEDULVIDIRMEDKREVIPYTHONLRLKWTGL 615

Db 2186 AVYEGSLVURGVEDVYVFGETYTFGW---TYDMENESDKYFVPEH---KACRG 2236

Oy 616 AGDRTKDFHE-----IELKNNQELLSOTVKIDTKNLEFKDKATINMK--HGE 663

Db 2237 NLJDDIKYFDEKGIMRGGLISBENNYY-----NENGEBIQGYINIEDKMFVGE 2288

Oy 664 SLRLQ---GLPREGYSYLVE 680

Db 2289 DGWMQIGVFTPDGFKFAHO 2309

RESULT 12  
T28679  
fibrinogen-binding protein homolog - Staphylococcus aureus

C;Species: Staphylococcus aureus

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-May-2000

C;Accession: T28679

R.; Josefsson, E.; McCrea, K.; Ni, Edhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T.; Microbiology, 144, 3387-3395, 1998  
A; Title: Three new members of the serine-aspartate repeat protein multigene family of St A; Reference number: Z20510; MUID:99098700; PMID:9884231  
A; Accession: F28679  
A; Status: preliminary; translated from GB/EMBL/DDBJ  
A; Molecule type: DNA  
A; Cross-references: EMBL:AJ005646; NID:e1318791; PID:e1318792; PIDN:CAA06651.1  
C; Genetics: srd

Db 466 VLRVKENNNSVATSKVVKDANKLTONGKVDFKDSLNSKEYITEMEKLVDGKEVTD 525  
 Qy 448 ---FTGEVK-YTHIAGRDLKYTVPRDT-----DPDFLKHKVV-TEGYREKG 494  
 Db 526 NWYFIASTLKKAPSMAGIDLSYSTEMKEFTAIPINLIDTDSNTIRVAYLEEDKANG 585  
 Qy 495 QAIE--YSGETETOLRATOLA-----IYFTDS----- 521  
 Db 586 ONAKEAVSYVNVASOKRTAVKVGRTVMDSDGNVYFAYISGNNQSDFTLATPVNAV 645  
 Qy 522 -----AELDKDKL-KDHGF-----GDMNDSTLAVAKILVEAQDSNPQ 560  
 Db 646 GLKSKEPVEFSIKEARODKLINTNEYFDAVINLYDNLTHPTLKLKSDAQCMYDGSPVA 705  
 Qy 561 LTLDFRFIPNPKNYQSLI----- 521  
 Db 706 TVDL---RNKNEITNLLEFGGLESETYVWMTASYNLDGGAGIMWDOLIGOSGVFOTK 761  
 Qy 598 EVIPVTHNLTRKTVGLAGDRTKDFHFEIELKNNKQELLSOTVKT-DKTN-----LEF 650  
 Db 762 EIAKVNTFETLESVTINQA-----EVNIKSEAKKLNANSANLKYDKKNNTLVKTVPL 814  
 Qy 651 KDGKATNLKHGESLTIQGLPBGSYIWKETDSEGYKVVKVNSQEAVANTVSKT---GIT 706  
 Db 815 NDDFNKLMTEGCVTYLGEELAINEKYLKVED---GLDSGMNOVPVEGQLVFKTKASPI 872  
 Qy 707 SDETLAFFENKEPWPVPTGVDOKINGLALIVIAGI 741  
 Db 873 DKVLVDYQPNK-----LKVGG-----LAGI 892

RESULT 14  
 G82875 hypothetical protein UW559 [imported] - Ureaplasma urealyticum  
 C;Species: Ureaplasma urealyticum  
 C;Accession: G82875  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000  
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor reference number: A82870  
 A;Accession: G82875  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-183 <GLA>  
 A;Cross-references: GB:AE002154; GB:AF222894; NID:96899557; PIDN:AAF30971.1; GSPDB:GN001  
 A;Experimental source: serovar 3; biovar 1  
 C;Genetics:  
 A;Gene: UW558  
 A;Genetic code: SGC3

Query Match 3.8%; Score 148.5; DB 2; Length 1883;  
 Best Local Similarity 19.1%; Pred. No. 2.7; Mismatches 276; Indels 277; Gaps 34;  
 Matches 155; Conservative 102; Mismatches 276; Indels 277; Gaps 34;

Qy 103 SYQVYCENLKKAF--PLGSSDVVKVKKHKGISTKFDYAMS----- 143  
 Db 951 NFDTSMFLNKTYFDHPMFTSNEKRWAEIRDAFMVKPDENITSKLDEKANASSVPPY 1010  
 Qy 144 ---PRIGDELNQK-----LRAVMYNGHPONANGIMSGLEPLINAIRYQEAWYYS 191  
 Db 1011 KKLVLQIIGEIDINKSFQDFKVALLTQYNAKINDKSKKEVSKLDPPELI-EIKKY- 1067  
 Qy 1912 DNAPISNPDESFKRESEBNLNUVTSQSL-----MROALKQOLIDPNAT 234  
 Db 1068 -----DKQDFRGVVKVNVVAQTFILNFADLEGNGNGKYFVKPKEKELYQNILT 1119  
 Qy 235 KMKPQVDP----- 262  
 Db 1120 KTKYESVSIIGIRPSYLMQNKTYSBOLFNKSMINLNEFGTIKLIVDRGDKDNKHLK 1179  
 Qy 263 QNLGGGLWLPKPTPQDPPMPNQPOTTSVLRKAIG-DYSLLEGATIQLGTGNWNS 321

Db 1180 DELTEKEIYPLMLTPAE-----AQAINFDYLKSNNSFTPLTEN-NG 1222  
 Qy 322 FQARVFSSNDIGERIELSDGTYTTELNSPAGYSIARAPIEVKEAGKVYTD--GKQI 378  
 Db 1223 SKFTYTKPKDIPSIEF-----MSVDPAK-YTIVENALSSSH 1258  
 Qy 379 ENPK---ETVEPVSV-----EAYND---PEFSVLT-----QWYAKF 411  
 Db 1259 ENRKWQYELKERRYDVKDFEEVNIKKQEAVKNTLLEFKQNLGFLDFGETESTDIFKF 1318  
 Qy 412 YYAKNKNGSSQVY---CFNADIKSPPDSEGDGKTMDFTGEVKYTH-LAGRDLFKYV 468  
 Db 1319 YKSKDFNPSELDKYKQFDGKLGLYGRFSGKMYKERRGSPKCEPDLTYNFGNPQNWKA 1378  
 Qy 469 KRDTD---PDPFLKHKVVKVIKGYRK----GOATEYS-GLT----- 503  
 Db 1379 KPNQKNVRTVDSTIKGIOLEIERKHNENTNLNGQLQYARGFTIYDPGSKDYGWL 1438  
 Qy 504 -----EQQLRAATOLATYFTDSAELDKKLUKYHFGDMNDSTLAVAKILV-EY 552  
 Db 1439 GSFGTISQSSELPNADETEVSSDVTYLINKRKYQECNEIG-----DYVNIAEVLJRDY 1493  
 Qy 553 AQ-----DSNPPOPLDL-DFFLPNPKYQSLIGTQHPELVDLDTIRMEDKKEV 601  
 Db 1494 VQTVFITSQNEIDLNPWVIGSLDFNTGNEYFSGDNTKWN-----ERLIP 1540  
 Qy 602 VTHNLTRKTVGLAGRTKDHH-----FEELKNN-----QELSLQTVK 642  
 Db 1541 VNNFLSYNTIALNTLFATNNYEKIQVLANGALNVYQKNQOLFDYLTKPOELESFNK 1600  
 Qy 643 TDKTNLEFKDGKATINLKHGESLTQGLPEGSYLVKETDSEGYKVVKVNSQEAVANTVSK 702  
 Db 1601 VRESELSNANEFLALL-TKTHDSDVNL-NSYFLTRLSPK-----SNSYIGK 1645  
 Qy 703 TGTFSD-----ETLAFFENKEPV 720  
 Db 1646 TRITNNESFFKDRWLKIIDWEIYDDNREPI 1675

RESULT 15  
 AF1489 cell wall-associated protein precursor wapa (B. subtilis) homolog lin0454 [imported]  
 C;Species: Listeria innocua  
 C;Accession: AF1489  
 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001  
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloechl, P.; Dominguez-Bernal, G.; Duchaoud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Kart, U.; Science, 294, 819-852, 2001  
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurakpat, G.; Madiueno, E.; Maitouram, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla,  
 A;Title: Comparative genomics of Listeria species.  
 A;Reference number: AB1077; MUID:2153729; PMID:11679669  
 A;Accession: AF1489  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-2167 <GLA>  
 A;Cross-references: GB:AL592022; PIDN:CA95686.1; PID:g16412895; GSPDB:GN001178  
 A;Experimental source: strain Clp11262  
 C;Genetics:  
 A;Gene: lin0454

Query Match 3.7%; Score 147.5; DB 2; Length 2167;  
 Best Local Similarity 19.0%; Pred. No. 3.8; Mismatches 179; Conservative 111; Mismatches 319; Indels 331; Gaps 46;  
 Matches 179; Conservative 111; Mismatches 319; Indels 331; Gaps 46;

Qy 47 AKVYFGI-----VESSTNAAINFDSSSYRWRGCGYESVVRGHPYKOF-RVARD--- 93  
 Db 562 AGSTFGRLNRLTRYLFRYQAVFPGGESPNSDLVAFYAMPTEK-PQAPVAKAVSNLAKRETG 619  
 Qy 94 -LRVNLLEGAS--RSYQVCFNLK--KAFLGSDSSVKKWYKHDGI-STKE---DYAM 142  
 Db 620 YVELNWERKSPMADGYKVLFENGKAYEEVDVGAET--KWTTONKGWMPTEKEIAEGYAL 676

Search completed: August 19, 2003, 15:22:29  
Job time : 48 secs

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